

SEQUENCE LISTING

<110> GALZI, JEAN-LUC
ALIX, PHILIPPE

<120> USE OF A FLUORESCENT PROTEIN FOR DETECTING INTERACTION
BETWEEN A TARGET PROTEIN AND ITS LIGAND

<130> 97AHCNRFLU

<140> 09/445,205
<141> 2000-01-07

<150> PCT/FR98/01136
<151> 1998-06-04

<150> FR 97/06977
<151> 1997-06-05

<160> 25

<170> PatentIn Ver. 2.1

<210> 1
<211> 798
<212> DNA
<213> Aeq

<220>
<221> CDS
<222> (1) .. (795)

<400> 1

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

ctg acc tac ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg aag 240
 Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80

cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
100 105 110	
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
115 120 125	
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
130 135 140	
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac	480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	
145 150 155 160	
ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc	528
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser	
165 170 175	
gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac ggc	576
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly	
180 185 190	
ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc ctg	624
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu	
195 200 205	
agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag ttc	672
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe	
210 215 220	
gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag tac	720
Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Tyr	
225 230 235 240	
tca gat ctc gag ctc aag ctt cga att ctg cag tcg acg gta ccg cgg	768
Ser Asp Leu Glu Leu Lys Leu Arg Ile Leu Gln Ser Thr Val Pro Arg	
245 250 255	
gcc cgg gat cca ccg gat cta gat aac tga	798
Ala Arg Asp Pro Pro Asp Leu Asp Asn	
260 265	
<210> 2	
<211> 265	
<212> PRT	
<213> Aequorea victoria	
<400> 2	
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
1 5 10 15	
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
20 25 30	

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220

Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Tyr
 225 230 235 240

Ser Asp Leu Glu Leu Lys Leu Arg Ile Leu Gln Ser Thr Val Pro Arg
 245 250 255

Ala Arg Asp Pro Pro Asp Leu Asp Asn
 260 265

<210> 3
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: spacer sequence

<400> 3
 Gly Gly Gly Gly Ser
 1 5

<210> 4
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Cyclopeptide

<400> 4
Gln Trp Phe Gly Leu Met
1 5

<210> 5
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 5
ggtcgccacc ctgtacaaga agggcgagg

29

<210> 6
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 6
cacgagagga tgtacaacct cgagcgacca gtcacc

36

<210> 7
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 7
gtacccagac accagcttagc agatctgaag cttcgccatc aggc

44

<210> 8
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 8
ggagagttcc aactcgagaa aagaaagaag ggcgaggag 39

<210> 9
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 9
gtcagctgtt tctgcggcgc gctaagcctg ggcctt 36

<210> 10
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 10
ttagttctaa actagcggcc gcactagtcc tccatgaaca cttcagcccc a 51

<210> 11
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 11
cttgaaccta tagcttagcct cgagtcagca ttggcgggag gg 42

<210> 12
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 12
cctgctgtct cagatctcat caccgtcc 28

<210> 13
<211> 47

<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide

<400> 13

cagatcattta gttgtacagg aaagatcttg aggatcctgg agtgaag

47

<210> 14

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide

<400> 14

ggcccaagct tatgtcagga tccggggat

29

<210> 15

<211> 30

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:
Oligonucleotide

<400> 15

cgtcccgctcg agtcacaaggc ccacagatat

30

<210> 16

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide

<400> 16

gttgacaaggc ttccgggatcc a

21

<210> 17

<211> 78

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide

<400> 17
acacacagagg gcagtagcaa tgaggatgac agcgaggcgt gccgcggaga ccttcattgg 60
atcccgaaac ttgtcaac 78

<210> 18
<211> 78
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 18
attgctactg ccctctgtgc tcctgcacat gcctcccat attcctcgga caccacacca 60
tgctgcttcg cctacatt 78

<210> 19
<211> 78
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 19
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gtaggcgaag cagcatgg 78

<210> 20
<211> 78
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 20
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gtaggcgaag cagcatgg 78

<210> 21
<211> 69
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 21

ctagctcatc tccagcgagt tgatgtactc ccgaacccat ttcttctctg ggttggcaca 60
aacttgacg 69

<210> 22
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 22
aactcgctgg agatgagcta ggccggccgct cgaggtcgac ctagtcacta 50

<210> 23
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 23
tagtgactag gtcgacacctcg a 21

<210> 24
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 24
gccccccgcat gggggatcct actctggagt ccatcatggc g 41

<210> 25
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 25
ccgctcgagt taatctagaa ggaccagatt gtactccttc agg 43